RAW SEQUENCE LISTING
PATENT APPLICATION US/09/235,416A

DATE: 04/26/2000
TIME: 18:32:15

Input Set: I235416A.RAW

P#10

This Raw Listing contains the General Information Section and up to first 5 pages.

<110> APPLICANT: Sakowicz, Roman
Goldstein, Lawrence S. B.
The Regents of the University of California
<120> TITLE OF INVENTION: Identification and Expression of a Novel Kinesin Motor Protein
<130> FILE REFERENCE: 18557C-000710US
<140> CURRENT APPLICATION NUMBER: US/09/235,416A
<141> CURRENT FILING DATE: 1999-01-22
<150> EARLIER APPLICATION NUMBER: WO PCT/US99/01355
<151> EARLIER FILING DATE: 1999-01-22
<150> EARLIER APPLICATION NUMBER: US 60/072,361
<151> EARLIER FILING DATE: 1998-01-23
<160> NUMBER OF SEQ ID NOS: 7
<170> SOFTWARE: PatentIn Ver. 2.0
<210> SEQ ID NO 1
<211> LENGTH: 784
<212> TYPE: PRT
<213> ORGANISM: Thermomyces lanuginosus
<220> FEATURE:
<223> OTHER INFORMATION: TL-gamma ATP-dependent plus end-directed microtubule motor protein
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)..(357)
<223> OTHER INFORMATION: kinesin-like microtubule motor domain
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (358)..(442)
<223> OTHER INFORMATION: neck domain links motor domain to stalk domain
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (443)..(601)
<223> OTHER INFORMATION: stalk domain, unc-104 family domain
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (602)..(784)
<223> OTHER INFORMATION: tail domain
<400> SEQUENCE: 1

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Gly Asn Gln Thr Ile Leu Thr Pro Pro Pro Gly Ala Glu Glu Lys Ala
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Gln Glu Asp Leu Phe Gln Asp Leu Gly Val Pro Leu Leu Asp Asn Ala
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Phe Lys Gly Tyr Asn Asn Cys Ile Phe Ala Tyr Gly Gln Thr Gly Ser
            100                 105                 110
Gly Lys Ser Tyr Ser Met Met Gly Tyr Gly Lys Glu His Gly Val Ile
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Pro Arg Ile Cys Gln Asp Met Phe Arg Arg Ile Asn Glu Leu Gln Lys
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Asp Lys Asn Leu Thr Cys Thr Val Glu Val Ser Tyr Leu Glu Ile Tyr
145                 150                 155                 160
Asn Glu Arg Val Arg Asp Leu Leu Asn Pro Ser Thr Lys Gly Asn Leu
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Lys Val Arg Glu His Pro Ser Thr Gly Pro Tyr Val Glu Asp Leu Ala
            180                 185                 190
Lys Leu Val Val Arg Ser Phe Gln Glu Ile Glu Asn Leu Met Asp Glu
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Gly Asn Lys Ala Arg Thr Val Ala Ala Thr Asn Met Asn Glu Thr Ser
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Ser Arg Ser His Ala Val Phe Thr Leu Thr Leu Thr Gln Lys Trp His
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Asp Glu Glu Thr Lys Met Asp Thr Glu Lys Val Ala Lys Ile Ser Leu
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Val Asp Leu Ala Gly Ser Glu Arg Ala Thr Ser Thr Gly Ala Thr Gly
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Ala Arg Leu Lys Glu Gly Ala Glu Ile Asn Arg Ser Leu Ser Thr Leu
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Gly Arg Val Ile Ala Ala Leu Ala Asp Met Ser Ser Gly Lys Gln Lys
    290                 295                 300
Lys Asn Gln Leu Val Pro Tyr Arg Asp Ser Val Leu Thr Trp Leu Leu
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Lys Asp Ser Leu Gly Gly Asn Ser Met Thr Ala Met Ile Ala Ala Ile
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Ser Pro Ala Asp Ile Asn Phe Glu Glu Thr Leu Ser Thr Leu Arg Tyr
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Ala Asp Ser Ala Lys Arg Ile Lys Asn His Ala Val Val Asn Glu Asp
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Lys Gln Ile Val Ser Ile Gln Gln Pro Asp Ala Thr Val Lys Lys Met
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Val Asn Leu Ser Asp Asp Pro Leu Leu Ala Glu Cys Leu Val Tyr Asn
500 505 510
Ile Lys Pro Gly Gln Thr Arg Val Gly Asn Val Asn Gln Asp Thr Gln
515 520 525
Ala Glu Ile Arg Leu Asn Gly Ser Lys Ile Leu Lys Glu His Cys Thr
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Phe Glu Asn Val Asp Asn Val Val Thr Ile Val Pro Asn Glu Lys Ala
545 550 555 560
Ala Val Met Val Asn Gly Val Arg Ile Asp Lys Pro Thr Arg Leu Arg
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Ser Gly Tyr Arg Ile Ile Leu Gly Asp Phe His Ile Phe Arg Phe Asn
580 585 590
His Pro Glu Glu Ala Arg Ala Glu Arg Gln Glu Gln Ser Leu Leu Arg
595 600 605
His Ser Val Thr Asn Ser Gln Leu Gly Ser Pro Ala Pro Gly Arg His
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Asp Arg Thr Leu Ser Lys Ala Gly Ser Asp Ala Asp Gly Asp Ser Arg
625 630 635 640
Ser Asp Ser Pro Leu Pro His Phe Arg Gly Lys Asp Ser Asp Trp Phe
645 650 655
Tyr Ala Arg Arg Glu Ala Ala Ser Ala Ile Leu Gly Leu Asp Gln Lys
660 665 670
Ile Ser His Leu Thr Asp Asp Glu Leu Asp Ala Leu Phe Asp Asp Val
675 680 685
Gln Lys Ala Arg Ala Val Arg Arg Gly Leu Val Glu Asp Asn Glu Asp
690 695 700
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Gly Thr Ile Asp Asn Phe Ser Leu Asp Thr Ala Ile Thr Met Pro Gly
725 730 735
Thr Pro Arg Ser Asp Asp Asp Gly Asp Ala Leu Phe Phe Gly Asp Lys
740 745 750
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: TL-gamma ATP-dependent plus end-directed microtubule motor protein
<400> SEQUENCE: 2

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147         cctccgggtg ccgaagagaa ggcgcgtaaa agtggcaaaa ctattatgga tggcccgaag 180
148         gcatttgcgt tcgatcggtc gtattggtcc tttgacaaga atgctcccaa ctatgcgaga 240
149         caggaagacc tattccaaga tctcggagtc ccgcttctgg ataatgcatt caagggttat 300
150         aacaattgta tcttcgccta cggtcagacc ggttcgggca agtcctattc aatgatgggc 360
151         tatggcaagg agcatggcgt gatcccgcgg atttgccagg acatgttccg gcgtattaat 420
152         gaactgcaga aggacaagaa cctcacttgc accgtcgaag tttcgtactt ggaaatttac 480
153         aatgaacgag tgcgagactt gctgaatccg.tcgacaaagg ggaatctcaa ggtccgagaa 540
154         cacccgtcga ccggccccta cgtggaggac ttggcgaagc tggtcgtgcg atcattccaa 600
155         gaaatcgaaa atctcatgga tgagggcaac aaagccagaa cggttgccgc cacaaacatg 660
156         aacgagacat ccagtcgatc ccacgccgtc ttcactttga ccttgacgca aaagtggcat 720
157         gatgaagaga ccaaaatgga cacagagaag gttgcgaaga tcagtctggt agatttggcg 780
158         ggttctgagc gagcaacgtc caccggagct actggagcgc gactgaagga gggtgcagag 840
159         atcaaccgct cactttcgac cctaggtcgt gtgattgcag cgctagcgga tatgtcgtcg 900
160         ggaaaacaga agaagaatca gttagtacct taccgagatt cggtactgac gtggcttctg 960
161         aaggactcct tgggaggcaa ctcgatgacc gccatgattg ccgccatttc gcctgctgat 1020
162         attaactttg aagagactct cagtaccctt cgatatgcgg actctgcgaa gcgaatcaag 1080
163         aaccacgcag tggtcaatga agacccgaac gcgcggatga tccgcgagtt gaaggaggaa 1140
164         ctcgcgcagc tgaggagcaa actccagagc agtggtggag gtggaggtgg tgcaggaggt 1200
165         tctggcgggc cagtggagga atcgtacccg cccgacacgc cgctcgagaa gcaaatcgtg 1260
166         tcgattcagc agccggatgc gacagtcaag aaaatgagca aggcagaaat cgtggagcaa 1320
167         ctgaaccaga gtgagaagct ctatcgggat ctcaatcaga cctgggaaga gaagctggcc 1380
168         aagaccgagg aaatccacaa ggaacgagaa gcggcgctcg aggagctggg tatcagcatc 1440
169         gaaaagggct ttgttggccc ttaccactcc aaagaaatgc cacatctagt caacttgagc 1500
170         gatgatcctc ttctggctga gtgtcttgtc tacaacatca agcccgggca gacaagggtt 1560
171         ggaaacgtca accaagatac acaagcggaa attcgtctga acggttcgaa gatcctgaaa 1620
172         gaacactgta cgtttgaaaa tgtggacaac gttgtgacca tcgtgccaaa cgagaaggct 1680
173         gctgtcatgg tgaacggcgt gcgaatcgac aagcctactc gcctccgcag cggctacagg 1740
174         atcatcctgg gcgatttcca cattttcga ttcaaccatc cggaagaagc tcgtgcggaa 1800
175         cggcaagaac aatccttgct tcgccattct gtcaccaaca gtcagttggg ttcgcctgct 1860
176         ccaggccgtc acgaccggac actgagcaag gcgggttcgg atgcggacgg cgattctcgc 1920
177         tcagattctc ctttgccgca ctttcgtgga aaggatagcg actggttcta tgctcgcagg 1980
178         gaagctgcta gcgcgatcct agggttggat cagaagatct ctcatctgac agatgacgag 2040
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186   <211> LENGTH: 21
187   <212> TYPE: DNA
188   <213> ORGANISM: Artificial Sequence
189   <220> FEATURE:
190   <223> OTHER INFORMATION: Description of Artificial Sequence:primer
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193   <210> SEQ ID NO 4
194   <211> LENGTH: 23
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196  <213> ORGANISM: Artificial Sequence
197  <220> FEATURE:
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202  <211> LENGTH: 30
203  <212> TYPE: DNA
204  <213> ORGANISM: Artificial Sequence
205  <220> FEATURE:
206  <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
207        forward primer
208  <220> FEATURE:
209  <221> NAME/KEY: modified_base
210  <222> LOCATION: (25)
211  <223> OTHER INFORMATION: n = a, c, g or t
212  <400> SEQUENCE: 5
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214  <210> SEQ ID NO 6
215  <211> LENGTH: 30
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217  <213> ORGANISM: Artificial Sequence
218  <220> FEATURE:
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221  <220> FEATURE:
222  <221> NAME/KEY: modified_base
223  <222> LOCATION: (16)
224  <223> OTHER INFORMATION: n = a, c, g or t
225  <220> FEATURE:
226  <221> NAME/KEY: modified_base
227  <222> LOCATION: (28)
228  <223> OTHER INFORMATION: n = a, c, g or t
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233  <212> TYPE: DNA
234  <213> ORGANISM: Artificial Sequence
235  <220> FEATURE:
236  <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
237        reverse primer
238  <220> FEATURE:
239  <221> NAME/KEY: modified_base
240  <222> LOCATION: (16)
241  <223> OTHER INFORMATION: n = a, c, g or t
242  <220> FEATURE:
243  <221> NAME/KEY: modified_base
244  <222> LOCATION: (28)
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

FYI

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/235,416A**

Input Set: **I235416A.RAW**

Line	?	Error/Warning	Original Text
213	W	"N" or "Xaa" used: Feature required	gcgcggatcc atyttygcht ayggncarac
230	W	"N" or "Xaa" used: Feature required	gcgcgaattc tcdganccdg cvarrtcnac
247	W	"N" or "Xaa" used: Feature required	gcgcgaattc tcdctnccdg cvarrtcnac